CLAIMS

1. A PCR primer comprising a first sequence of a given base length which is complementary to one of single strands of target DNA and a second sequence which is provided adjacent to the side of 5′ terminus of said first sequence, has a GA or GC sequence at the side of 5′ terminus and is non-complementary to the single strand of said target DNA.

2. A method for executing PCR amplification comprising subjecting target DNA to PCR amplification with a first PCR primer which has a first sequence of a given base length complementary to one of single strands of target DNA, a GA or GG sequence at the side of 5′ terminus provided adjacent to the side of at 5′ terminus of said first sequence, and a second sequence non-complementary to said target DNA, and a second PCR primer having a third sequence of a given base length complementary to the other single strands of said target DNA.

3. A PCR primer according to Claim 1, wherein the base length of said first sequence is at 12 to 20.

4. A method for executing PCR amplification according to Claim 2, wherein said second PCR primer or both of said first and second primers are fluorescence labeled.

5. A method for analyzing a DNA fragment comprising the steps of PCR amplification using a first PCR primer having a first sequence of a given base

length which is complementary to one of single strands of target DNA and a second sequence which has a GA or GG sequence at 5′ terminus provided adjacent to the side of 5′ terminus of said first sequence and a second sequence non-complementary to said target DNA and a second PCR primer having a third sequence of a given base length which is complementary to one of other strands of said target DNA, and also using a thermostable DNA polymerase having terminal transferase activity, and detecting an amplified DNA fragment by electrophoresis.

6. A method for deciding a base sequence of a primer comprising providing four types of primers which, respectively, have a structure comprising a first sequence of a given base length complementary to one of single strands of target DNA and a second sequence of a given base length non-complementary to said one single strand provided adjacent to the side of 5′ terminus of said first sequence and which, respectively have, at 5′ terminus of said second sequence, one base whose types differ from one another, carrying out PCR by use of the four types of primers, analyzing the results of amplified products obtained by the PCR to obtain efficiencies of adenylation thereof, and deciding said second sequence as a sequence which is most likely to undergo adenylation.

7. A method for deciding a base sequence of a primer according to Claim 6, which comprises selecting

one base at the 5′ terminus of said second sequence, providing four types of primers which, respectively, have one base shifted from the 5′ terminus by one base toward the side of 3′ terminus and individual bases differ in type from one another, carrying out PCR by use of the four types of primers, analyzing the results of amplified products by the PCR to determine efficiencies of adenylation, from which the one base shifted from the 5′ terminus by one base toward the 3′ terminus is decided, optionally further providing four types of primers wherein the types of bases differ from each other with respect to one base shifted further by one base toward the3′ terminus and carrying out PCR the last-mentioned four types of primers, analyzing the results of amplified product by the last-mentioned PCR to obtain efficiencies of adenylation, and successively deciding said second sequence as one which is most likely to undergo adenylation.

8. A method for deciding a base sequence of a primer, which comprises providing four types of primers which, respectively, have a structure comprising a first sequence of a given base length complementary to one of single strands of DNA and a second sequence of a given base length non-complementary to said one single strand provided adjacent to the side of 5′ terminus of said first sequence and which, respectively have, at 5′ terminus of said second sequence, one base whose types differ from one another, carrying out PCR by use of the

four types of primers, analyzing the results of amplified product obtained by the PCR to determine said second sequence as a sequence that is most likely to undergo adenylation whereby a second sequence that is most likely to undergo adenylation is preliminarily prepared, and checking, when target DNA is provided, whether or not a primer composed of a combination of the first sequence of a given base length complementary to one of single strands of said target DNA and the preliminarily prepared second sequence has a stable secondary structure.

9. A service using the method defined in Claim 8, wherein a base sequence which is likely to undergo adenylation with and is non-complementary to given target DNA is researched by use of the method of deciding a base sequence of a primer recited in Claim 8, designing a base sequence of a primer having the non-complementary base sequence, and providing a base sequence for said primer.